



Score (bits)	E Value	
Sequences producing significant alignments:		
gi 55642389 ref XP_523094.1 PREDICTED: similar to Presenil...	452	e-126
gi 37182518 gb AAQ89061.1 TAAV688 [Homo sapiens]	451	e-125
gi 50726954 ref NP_112591.2 presenilin stabilization facto...	449	e-125
gi 12052866 emb CAB66606.1 hypothetical protein [Homo sapi...	447	e-124
gi 55726744 emb CAH90134.1 hypothetical protein [Pongo pyg...	444	e-123
gi 29243936 ref NP_808251.1 hypothetical protein 4632417K0...	391	e-107
gi 34864291 ref XP_217185.2 similar to RIKEN cDNA 0610008A...	377	e-103
gi 21492616 ref NP_080950.1 RIKEN cDNA 0610008A10 [Mus mus...	369	e-101
gi 37682171 gb AAQ98012.1 anterior pharynx defective 1B-li...	284	2e-75
gi 34864287 ref XP_343418.1 similar to RIKEN cDNA 0610008A...	282	7e-75
gi 17389295 gb AAH17699.1 APH-1A protein [Homo sapiens] >g...	256	7e-67
gi 15990414 gb AAH15568.1 APH-1A protein [Homo sapiens] >g...	254	2e-66
gi 12654775 gb AAH01230.1 APH-1A protein [Homo sapiens]	254	2e-66
gi 56268871 gb AAH87081.1 Unknown (protein for MGC:94545) ...	253	5e-66
gi 22203751 ref NP_666216.1 anterior pharynx defective 1A ...	252	8e-66
gi 34858248 ref XP_345252.1 similar to Aph1a-pending prote...	252	1e-65
gi 18848275 gb AAH24111.1 6530402N02Rik protein [Mus muscu...	251	2e-65

gi 7705787 ref NP_057106.1	CGI-78 protein [Homo sapiens] >...	248	2e-64	G
gi 26324468 dbj BAC25988.1	unnamed protein product [Mus mu...]	246	6e-64	G
gi 47214485 emb CAG12490.1	unnamed protein product [Tetrao...]	211	3e-53	
gi 48095709 ref XP_392345.1	similar to CG2855-PA [Apis mel...]	178	1e-43	G
gi 54644318 gb EAL33059.1	GA15487-PA [Drosophila pseudoobs...]	172	1e-41	
gi 20129183 ref NP_608710.1	CG2855-PA [Drosophila melanoga...]	164	3e-39	G
gi 55236032 gb EAA14158.3	ENSANGP00000015809 [Anopheles ga...]	164	4e-39	
gi 26347159 dbj BAC37228.1	unnamed protein product [Mus mu...]	162	1e-38	G
gi 31233667 ref XP_318923.1	ENSANGP00000015809 [Anopheles ...]	158	2e-37	G
gi 50806123 ref XP_428797.1	PREDICTED: similar to Anterior...	154	3e-36	G
gi 56204871 emb CAI22813.1	likely ortholog of C. elegans a...	145	1e-33	
gi 50809568 ref XP_429030.1	PREDICTED: similar to anterior...	121	3e-26	G
gi 39580694 emb CAE70374.1	Hypothetical protein CBG16933 [...]	81	4e-14	
gi 17509423 ref NP_492469.1	i-78 protein like, Anterior PH...	74	7e-12	G
gi 50252282 dbj BAD28287.1	presenilin stabilization factor...	71	3e-11	
gi 20453379 gb AAM19928.1	At2g31440/T28P16.7 [Arabidopsis ...]	70	6e-11	G
gi 21594204 gb AAM65980.1	unknown [Arabidopsis thaliana]	69	1e-10	
gi 56500904 emb CAH94855.1	conserved hypothetical protein ...	37	0.90	
gi 22024126 ref NP_610786.2	CG8545-PA [Drosophila melanoga...]	36	1.5	G
gi 32403290 ref XP_322258.1	hypothetical protein [Neurospo...]	35	2.0	G
gi 9837379 gb AAG00551.1	retinitis pigmentosa GTPase regul...	35	2.0	
gi 31621286 tpg DAA01153.1	TPA: RT11 [Mus musculus] >gi 46...	35	2.6	G
gi 2209198 gb AAB61441.1	LOX6 [Helobdella robusta]	35	2.6	
gi 32414609 ref XP_327784.1	hypothetical protein [Neurospo...]	35	3.4	G
gi 55588200 ref XP_513809.1	PREDICTED: hypothetical protei...	35	3.4	
gi 51458782 ref XP_371313.2	PREDICTED: similar to dJ14N1.2...	35	3.4	G
gi 12314268 emb CAC13173.1	novel S-100\ICaBP type calcium...	35	3.4	
gi 32423411 ref XP_332143.1	predicted protein [Neurospora ...]	34	4.5	G
gi 53719504 ref YP_108490.1	putative lipoprotein [Burkhold...	34	4.5	G
gi 53723509 ref YP_102951.1	TPR domain protein [Burkholder...	34	4.5	G
gi 42554029 gb EAA76872.1	hypothetical protein FG07524.1 [...]	34	5.8	
gi 46444603 gb EAL03877.1	hypothetical protein Ca019.1574 ...	34	5.8	
gi 46444453 gb EAL03728.1	hypothetical protein Ca019.9147 ...	34	5.8	
gi 56315671 emb CAI10315.1	hypothetical protein [Azoarcus ...]	34	5.8	
gi 46228566 gb EAK89436.1	hypothetical protein with possib...	34	5.8	
gi 7488765 pir T10863	extensin precursor - kidney bean >gi...	23	7.0	
gi 41054255 ref NP_956076.1	nuclear autoantigenic sperm pr...	33	7.6	G
gi 51557560 ref YP_068394.1	putative ORF-3 protein [Suid h...]	33	7.6	G
gi 22328344 ref NP_680595.1	hypothetical protein [Arabidop...]	33	7.6	G
gi 32563629 ref NP_491994.2	chromo domain and SNF2 related...	33	9.9	G
gi 23508533 ref NP_701202.1	hypothetical protein [Plasmodi...]	33	9.9	G
gi 55741482 ref NP_055840.1	myelin transcription factor 1...	33	9.9	G
gi 51708299 ref XP_143396.3	PREDICTED: similar to dJ14N1.2...	33	9.9	G
gi 50418016 gb AAH77951.1	Irx2-A protein [Xenopus laevis]	33	9.9	
gi 7504867 pir T23056	hypothetical protein H06001.2 - Caen...	33	9.9	
gi 9837383 gb AAG00553.1	retinitis pigmentosa GTPase regul...	33	9.9	

Alignments

Get selected sequences Select all Deselect all

>gi|55642389|ref|XP_523094.1| PREDICTED: similar to Presenilin stabilization factor [troglodytes]
Length = 389

Score = 452 bits (1162), Expect = e-126
Identities = 231/259 (89%), Positives = 231/259 (89%)
Frame = +3

Query: 3 VAMTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGXXXXXXXXXXXXMARV 182
VAMTAAVFFGCAFIAGPALALYVFTIA EPLRIIFLIAGA MARV

Sbjct: 131 VAMTAAVFFGCAFIAGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARV 190

Query: 183 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY 362
IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY

Sbjct: 191 IIDNKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAY 250

Query: 363 VSGLGFGIMSGVFSVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFF 542
VSGLGFGIMSGVFSVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFF

Sbjct: 251 VSGLGFGIMSGVFSVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFF 310

Query: 543 DGCEKKKGXXXXXXXXXXXXSAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRL 722
DGCEKKKG SAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRL

Sbjct: 311 DGCEKKKGILLIVLLTHLLVSAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRL 370

Query: 723 KLCLLCQDKNFLYNQRSR 779
KLCLLCQDKNFLYNQRSR

Sbjct: 371 KLCLLCQDKNFLYNQRSR 389

>gi|37182518|gb|AAQ89061.1|  TAAV688 [Homo sapiens]
Length = 257

Score = 451 bits (1159), Expect = e-125
Identities = 230/257 (89%), Positives = 230/257 (89%)
Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGXXXXXXXXXXXXMARVII 188
MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGA MARVII

Sbjct: 1 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVII 60

Query: 189 DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS

Sbjct: 61 DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 120

Query: 369 GLGFIMSGVFSVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDG 548
GLGFIMSGVFSVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDG

Sbjct: 121 GLGFIMSGVFSVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDG 180

Query: 549 CEKKKGXXXXXXXXXXXXSAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRLK 728
CEKKKG SAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRLK

Sbjct: 181 CEKKKGILLIVLLTHLLVSAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRLK 240

Query: 729 CLLCQDKNFLYNQRSR 779
CLLCQDKNFLYNQRSR

Sbjct: 241 CLLCQDKNFLYNQRSR 257

[>gi|50726954|ref|NP_112591.2|] [G] presenilin stabilization factor-like [Homo sapiens]
 gi|18088649|gb|AAH20905.1| [G] Presenilin stabilization factor-like [Homo sapiens]
 Length = 257

Score = 449 bits (1154), Expect = e-125
 Identities = 229/257 (89%), Positives = 229/257 (89%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGPALALYVFTIATEPLRIIFLIAGAFFWLVSLISSLVWFMARVII 60

Query: 189 DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368
 DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS
 Sbjct: 61 DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 120

Query: 369 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDG 548
 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDG 180

Query: 549 CEKKKGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLYNQRSR 779
 CLLCQDKNFLYNQRSR
 Sbjct: 241 CLLCQDKNFLYNQRSR 257

[>gi|12052866|emb|CAB66606.1|] [G] hypothetical protein [Homo sapiens]
 gi|37077447|sp|Q8WW43|AP1B_HUMAN [G] Gamma-secretase subunit APH-1B (APH-1b) (Aph-1
 stabilization factor-like)
 gi|24637564|gb|AAN63817.1| [G] presenilin stabilization factor-like protein [Homo sapiens]
 Length = 257

Score = 447 bits (1150), Expect = e-124
 Identities = 228/257 (88%), Positives = 229/257 (89%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGPALALYVFTIATEPLRIIFLIAGAFFWLVSLISSLVWFMARVII 60

Query: 189 DNKDGPQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368
 DNKDGPQKYLLIFGAFVSVYI+EMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS
 Sbjct: 61 DNKDGPQKYLLIFGAFVSVYIREMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 120

Query: 369 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDG 548
 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDG 180

Query: 549 CEKKKGXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLYNQRSR 779
 CLLCQDKNFLYNQRSR
 Sbjct: 241 CLLCQDKNFLYNQRSR 257

[>] >gi|55726744|emb|CAH90134.1| hypothetical protein [Pongo pygmaeus]
 Length = 257

Score = 444 bits (1142), Expect = e-123
 Identities = 226/257 (87%), Positives = 228/257 (88%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGPALALYVFTIA EPLRIIFLIAGA MARVII
 Sbjct: 1 MTAAVFFGCAFIAGPALALYVFTIATEPLRIIFLIAGAFFWLVSLLISLWVFMARVII 60

Query: 189 DNKDGPQKYLIFGAFVSVYIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLAYVS 368
 DNKDGPQKYLIFG FVSVYIQEMFRFAYY+LLKKASEGLKSINPGETAPSMRLAYVS
 Sbjct: 61 DNKDGPQKYLIFGTFVSVYIQEMFRFAYYRLLKASEGLKSINPGETAPSMRLAYVS 120

Query: 369 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSQPFFLYSAFMTLVIIILLHVFWGIVFFDG 548
 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSQPFFLYSAFMTLVIIILLHVFWGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSQPFFLYSAFMTLVIIILLHVFWGIVFFDG 180

Query: 549 CEKKKGXXXXXXXXXXXXAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEKKKG SAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL
 Sbjct: 181 CEKKKGILLIVLLTHLLVSAQTFIISYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 240

Query: 729 CLLCQDKNFLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLFLYNQRSR 257

[>] >gi|29243936|ref|NP_808251.1| [G] hypothetical protein 4632417K02 [Mus musculus]
 gi|50927492|gb|AAH79659.1| [G] Hypothetical protein 4632417K02 [Mus musculus]
 gi|26340556|dbj|BAC33940.1| [G] unnamed protein product [Mus musculus]
 gi|37077156|sp|Q8C7N7|AP1B_MOUSE [G] Gamma-secretase subunit APH-1B
 Length = 257

Score = 391 bits (1004), Expect = e-107
 Identities = 194/257 (75%), Positives = 210/257 (81%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGPALALYVFTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAAVFFGCAFIAGPALALYVFTIATDPLRVIFLIAGAFFWLVSLLSSVFWFLVRVIT 60

Query: 189 DNKDGPQKYLIFGAFVSVYIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYYKLLKASEGLKSINP ETAPSMRLAYVS
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYKLLKASEGLKSINPEETAPSMRLAYVS 120

Query: 369 GLGFGIMSGVFSVNTLSDSLGPCTVGIHGDSQPFFLYSAFMTLVIIILLHVFWGIVFFDG 548
 GLGFGIMSGVFSVNTLS+SLGPCTVGIHGDSQPFFL SAFMTLV+I+LHVFWG+VFFDG
 Sbjct: 121 GLGFGIMSGVFSVNTLSNSLGPCTVGIHGDSQPFFLNSAFMTLVVIMLHVFWGVFFDG 180

Query: 549 CEKKKGXXXXXXXXXXXXAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSLKL
 Sbjct: 181 CEKNKWYTLTVLLTHLVVSTQTFLSPYYEVNLVTAYIIMVLMGIWAFYVAGGSCRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

[gi|34864291|ref|XP_217185.2] G similar to RIKEN cDNA 0610008A10 [Rattus norvegicus]
 Length = 257

Score = 377 bits (968), Expect = e-103
 Identities = 189/257 (73%), Positives = 207/257 (80%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXMARVII 188
 MTA VFFGCAFIAFGPALALY+FTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAPVFFGCAFIAFGPALALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPQKYLLIFGAFVSFYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKASEGLKSINP ETAPSMRLLAYVS
 Sbjct: 61 DNRDGPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKASEGLKSINPEETAPSMRLLAYVS 120

Query: 369 GLGFGIMSGVFSVNTLSDSLPGPTVGIHGDSQPFFLYSAFM TLVII LHVFWGIVFFDG 548
 GLGFGIMSGVFSVNTLS++LGPGTVGIHGDSQPFFL SAFMTLVII+LHVFWGIVFFDG
 Sbjct: 121 GLGFGIMSGVFSVNTLSNALGPCTVGIHGDSQPFFLNSAFMTLVIIMLHVFWGIVFFDG 180

Query: 549 CEKKKGXXXXXXXXXXXXAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKL 728
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL
 Sbjct: 181 CEKNKWYILLTVLLTHLVVSTQTLLSPHYEVNLVTAYIIMVLMGIWAFCVAGGSRRSLKL 240

Query: 729 CLLCQDKNFLLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 CLLCQDKDFLLYNQRSR 257

[gi|21492616|ref|NP_080950.1] G RIKEN cDNA 0610008A10 [Mus musculus]
 gi|38648719|gb|AAH63254.1| G RIKEN cDNA 0610008A10 [Mus musculus]
 gi|29747906|gb|AAH50923.1| G RIKEN cDNA 0610008A10 [Mus musculus]
 gi|37077773|sp|Q9DCZ9|AP1C_MOUSE Putative gamma-secretase subunit APH-1C
 gi|12832198|dbj|BAB22004.1| G unnamed protein product [Mus musculus]
 Length = 258

Score = 369 bits (948), Expect = e-101
 Identities = 186/258 (72%), Positives = 204/258 (79%), Gaps = 1/258 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXMARVII 188
 MT VFFGCAFIAFGPA ALY+FTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTLPVFFGCAFIAFGPAFALYLFTIATDPLRVIFLIAGAFFWLVSLLLSSMFWFLVRVIT 60

Query: 189 DNKDGPQKYLLIFGAFVSFYIQEMFRFAYYKLLKKASEGLKSINPGET-APSMRLLAYV 365
 +N+D Q YLLIFGA +SV IQE+FR AYYKLLKKASEGLKSINP E APSMRLLAYV
 Sbjct: 61 NNRDESVQNYLLIFGALLSVCIQELFRLAYYKLLKKASEGLKSINPEEDIAPSMRLLAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLGPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFVGIVFFD 545
 SGLGFGIMSGVFSFVNTLS+SLGPGTVGIHGDSPQFFL SAFMTLV+I+LHVFWG+VFFD
 Sbjct: 121 SGLGFGIMSGVFSFVNTLSNSLGPGTVGIHGDSPQFFLNSAFMTLVVIMLHVFWGVVFFD 180

Query: 546 GCEKKKGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAAGGSCRSLK 725
 GCEK KW S QTF+S YY +NL +A+II+VLMG WAF AGGSCRSLK
 Sbjct: 181 GCEKNKWYTLTLLTVLLTHLVVSTQTFLSPYYEVNLVTAYIMVLMGIWAFYVAGGSCRSLK 240

Query: 726 LCLLCQDKNFLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 241 FCLLCQDKDFLFLYNQRSR 258

[>gi|37682171|gb|AAQ98012.1] [G] anterior pharynx defective 1B-like [Danio rerio]
 gi|41056229|ref|NP_956409.1| [G] anterior pharynx defective 1B [Danio rerio]
 gi|22001127|gb|AAM88325.1| [G] Aph-1 protein [Danio rerio]
 gi|47939453|gb|AAH71492.1| [G] Anterior pharynx defective 1B [Danio rerio]
 gi|37077309|sp|Q8JHE9|AP1B_BRARE Gamma-secretase subunit Aph-1b (Anterior-pharynx
 1b)
 Length = 258

Score = 284 bits (726), Expect = 2e-75
 Identities = 147/259 (56%), Positives = 183/259 (70%), Gaps = 2/259 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALARLYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXMARVII 188
 MT AVFFGC FIAFGPA+AL++FTIA +PLR+IFLIAGA + V I
 Sbjct: 1 MTVAVFFGCTFIAFGPAIALFMFTIARDPLRVIFIAGAFFWLVSLLLSSLVWFIT-VQI 59

Query: 189 DNKDGPQKY-LLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLLAY 362
 NK+ TQ+ LLIFG +SV +QE FR+ YY+LLKKA+EGL +++ +T P SMR LAY
 Sbjct: 60 SNKNSATQQQRGLLIFGVVLSVLLQEAFRYGYYRLLKKANEGLLALSQEDTMPISMRLQAY 119

Query: 363 VSGLGFGIMSGVFSFVNTLSDSLGPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFVGIVFF 542
 VSGLGFG MSG FS VN LSDSLGPGTVGIHG+S +F+ SAFMTL IILLH+FWG+VFF
 Sbjct: 120 VSGLGFGFMMSGAFSVVNILSDSLGPGTVGIHGESQHYFISSAFMTLAIILLHMFVGVVFF 179

Query: 543 DGCEKKKGXXXXXXXXXXXXXSAQTFISSYYGINLASAFIILVLMGTWAAGGSCRSL 722
 + CE++W S TF++ +Y +L +IIL +M WA+L AGGS R+L
 Sbjct: 180 EACERQRWWALGAVVASHLTVSCLTFVNPHYQGSLIPTYIILSVMWAYLCAGGSLRNL 239

Query: 723 KLCLLCQDKNFLYNQRSR 779
 KLCL C+DK+FLL N R R
 Sbjct: 240 KLCLTCKDKDFLLANHRPR 258

[>gi|34864287|ref|XP_343418.1] [G] similar to RIKEN cDNA 0610008A10 [Rattus norvegicus]
 Length = 216

Score = 282 bits (722), Expect = 7e-75
 Identities = 151/257 (58%), Positives = 168/257 (65%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALARLYVFTIAIEPLRIIFLIAGAXXXXXXXXXXXMARVII 188
 MTAAVFFGCAFIAGPALARLYVFTIA +PLR+IFLIAGA + RVI
 Sbjct: 1 MTAAVFFGCAFIAGPALSLEYVFTIATDPLRVIFIAGAFFWLVSLLLSSVFWFLVRVIT 60

Query: 189 DNKDGPQTQYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVS 368
 DN+DGP Q YLLIFG +SV IQE+FR AYY+LLKKA+EGLKSINP ETAPSMRLAY
 Sbjct: 61 DNRDPVQNYLLIFGVLLSVCIQELFRLAYYRLLKKANEGLKSINPEETAPSMRLAY-- 118

Query: 369 GLGFGIMSGVFSFVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDG 548
 AFMTLVII+LHVFWGIVFFDG
 Sbjct: 119 -----AFMTLVIIIMLHVFWGIVFFDG 139

Query: 549 CEKKKGXXXXXXXXXXXXAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLK 728
 CEK KW S QT +S +Y +NL +A+II+VLMG WAF AGGS RSLKL
 Sbjct: 140 CEKNKWKYILLTVLLTHLLVSTQTLSPHYEVNLVTAYIIMVLMGIWAFCVAGGSRRSLKL 199

Query: 729 CLLCQDKNFLYNQRSR 779
 CLLCQDK+FLLYNQRSR
 Sbjct: 200 CLLCQDKDFLLYNQRSR 216

[>gi|17389295|gb|AAH17699.1| G] APH-1A protein [Homo sapiens]
 gi|14250557|gb|AAH08732.1| G] APH-1A protein [Homo sapiens]
 gi|14550502|gb|AAH09501.1| G] APH-1A protein [Homo sapiens]
 gi|37183020|gb|AAQ89310.1| G] GAAV579 [Homo sapiens]
 gi|56204870|emb|CAI22812.1| likely ortholog of C. elegans anterior pharynx defect
 (APH-1A) [Homo sapiens]
 gi|25989508|gb|AAM61955.1| G] presenilin stabilization factor a [Homo sapiens]
 gi|22761292|dbj|BAC11529.1| G] unnamed protein product [Homo sapiens]
 Length = 247

Score = 256 bits (653), Expect = 7e-67
 Identities = 129/247 (52%), Positives = 166/247 (67%), Gaps = 1/247 (0%)
 Frame = +3

Query: 9 MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAAGXXXXXXXXXXXXMARVII 188
 M AAVFFGC F+AFGPA AL++ T+A +PLR+I L+AGA + +
 Sbjct: 1 MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVT 60

Query: 189 DNKDGPQTQYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAP-SMRLAYV 365
 D D Q LLIFGA VSV +QE+FRFAYYKLLKA EGL S++ +P S+R +AYV
 Sbjct: 61 DRSDARLQYGLLIFGAAVSLLQEVFRFAYYKLLKADEGLASLSEDGRSPISIORMAYV 120

Query: 366 SGLGFGIMSGVFSFVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFD 545
 SGL FGI+SGVFS +N L+D+LGPG VGIHGDSP +FL SAF+T IILLH FWG+VFFD
 Sbjct: 121 SGLSFGIISGVFSVINILADALGPGVVGHIHGDSPYFLTS AFLTAIIILLHTFWGVVFFD 180

Query: 546 GCEKKKGXXXXXXXXXXXXAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLK 725
 CE++++ S TF++ +Y +L + + V MG WAF AGGS RS++
 Sbjct: 181 ACERRRYWALGLVVGSHLLTSGLTFNPWEASLLPIYAVTSMGLWAFITAGGSLRSIQ 240

Query: 726 LCLLCQD 746
 LLC+D
 Sbjct: 241 RSLLCKD 247

[>gi|15990414|gb|AAH15568.1| G] APH-1A protein [Homo sapiens]
 gi|18088501|gb|AAH20590.1| G] APH-1A protein [Homo sapiens]